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<!--StartFragment-->US-10-179-373-17
; Sequence 17, Application US/10179373
; Publication No. US20030232407A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: LI, XIAODONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: O'CONNELL, SHAWN
; APPLICANT: ZOZULYA, SERGEY
; APPLICANT: ADLER, JON
; APPLICANT: XU, HONG
; APPLICANT: ECHEVERRI, FERNANDO
; TITLE OF INVENTION: T1R HETERO-OLIGOMERIC TASTE RECEPTORS AND CELL LINES
; TITLE OF INVENTION: THAT EXPRESS SAID RECEPTORS AND USE THEREOF FOR
; TITLE OF INVENTION: IDENTIFICATION OF TASTE COMPOUNDS
; FILE REFERENCE: 078003-0291566
; CURRENT APPLICATION NUMBER: US/10/179,373
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: 60/300,434
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/304,749
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/310,493
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/331,771
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/339,472
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/372,090
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/374,143
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-179-373-17

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Query Match 91.9%; Score 4134; DB 4; Length 843;
 Best Local Similarity 91.0%; Pred. No. 0;
 Matches 767; Conservative 34; Mismatches 42; Indels 0; Gaps 0;

Qy	1 MGPQARTLHLLFLLLHALPKPVMLVGNSDPHLAGDYLLGGLPTLHANVKSVSHLSYLQVP 60
Db	1 MGPQARTLCLLSLLHVLPKPGKLVENSDPFLAGDYLLGGLPTLHANVKSISHLSYLQVP 60
Qy	61 KCNEYNMVKVLGYNLMQAMRFAVEEINNCSSLLPGVLLGYEMDV CYLSNNIOPGLYPLSQ 120
Db	61 KCNEPTMKVLGYNLMQAMRFAVEEINNCSSLLPGVLLGYEMDV CYLSNNIHPGLYPLAQ 120
Qy	121 IDDFPLILKDYSQYRPQVVAVIGPDNSESAITVSNILSYPLVPQVTYSAITDKLQDKRRP 180
Db	121 DDDLLPLILKDYSQYMPHVVAVIGPDNSESAITVSNILSHPLIPQITYSAISDKLRDKRHF 180
Qy	181 PAMLRTVPSATHHIEAMVQLMVHPQWNWIVVVLVSDDDYGRENSHLLSQLTLNTGDICIAF 240
Db	181 PSMLRTVPSATHHIEAMVQLMVHPQWNWIVVVLVSDDDYGRENSHLLSQLTLKTSDCIAF 240
Qy	241 QEVLPVPEPNQAVRPEEQDQLDNILDKLRRTSARVVIFSPELS LHNFREVLRWNFTGP 300
Db	241 QEVLPPIPESQVMRSEEQRQLDNILDKLRRTSARVVVFSPELS LYSPFFHEVLRWNFTGP 300
Qy	301 VWIASESWAIDPVLNLTTELRTGTPLGVTIQRVSIPGFSQPRVRHDKGYRMPNETSLR 360
Db	301 VWIASESWAIDPVLNLTTELRTGTPLGVTIQRVSIPGFSQPRVRDKPGYPVPTTSLR 360
Qy	361 TTCNQDCDACMNITESPNNVMLSGERVVSVYSAVYAVAHTLHRLLLCNQVRCTKQIVY 420
Db	361 TTCNQDCDACLNNTKSFNNILILSGERVVSVYSAVYAVAHLHRLLGNCNRVRCRKQKVY 420
Qy	421 PWQLLREIWHVNPTLLGNQLFPDEQGDMPMLLDIIQWQWGLSQNPPQSIASYSPTETRLT 480
Db	421 PWQLLREIWHVNPTLLGNRLFPDQQGDMPMLLDIIQWQWDLSQNPPQSIASYSPTSKRLT 480
Qy	481 YINNSWYTPNNTVPISMCSKSCQPGQMKKPIGLHPCCFECVDCPPDTYLNRSVDEFNCL 540
Db	481 YINNSWYTPNNTVPVSMCSKSCQPGQMKKSVGLHPCCFECLDMPGTYLNRSADEPNCL 540
Qy	541 SCPGSMWSYKNNIACPKRRLAPLEWHEVPTIVVTILAALGPISTLAILLIPWRHPQTPMV 600

Db 541 SCPGSMWSYKNDITCPQRPTFLEWHEVPTIVAILAALGFFSTLAILPIFWRHPQTPMV 600
Qy 601 RSAGGPMCPMLVPLLLAEGMVPVYVGPPTVPSFCRQAPPTVCPSVCLSCITVRSPQIV 660
Db 601 RSAGGPMCPMLVPLLLAEGMVPVYVGPPTVPSFCRQAPPTVCPSICLSCITVRSPQIV 660
Qy 661 CVFKMARRLPSAYGFWMRYHGPYVFVAPITAVKVALVAGNMLATTINPIGRTDPDDPNII 720
Db 661 CVFKMARRLPSAYSPWMRYHGPYVFVAPITAIKVALVVGNNMLATTINPIGRTDPDDPNIM 720
Qy 721 ILSCHPNYRNGLLFNTSMDLLSVLGFSPAYVGKELPTNYNEAKFITLSMTFSPTSSISL 780
Db 721 ILSCHPNYRNGLLFNTSMDLLSVLGFSPAYMGKELPTNYNEAKFITLSMTFSPTSSISL 780
Qy 781 CTFMSVHDGVLVТИMDLLTVLNFLAIGLGYFGPKCYMILPYPERNTSAYFNSMIQGYTM 840
Db 781 CTFMSVHDGVLVТИMDLLTVLNFLAIGLGYFGPKCYMILFYPERNTSAYFNSMIQGYTM 840
Qy 841 RKS 843
Db 841 RKS 843

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Query Match 100.0%; Score 4494; DB 4; Length 843;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MGPQARTLCLLSLLLHVLPKPGKLVENSDPHLAGDYLLGGLPTLHANVKSISHLSYLQVP 60
Db	1 MGPQARTLCLLSLLLHVLPKPGKLVENSDPHLAGDYLLGGLPTLHANVKSISHLSYLQVP 60
Qy	61 KCNEPTMKVLGYNLMQAMRPAVEEINNCSSLPGVLLGYEMDV CYLSNNIHPGLYPLAQ 120
Db	61 KCNEPTMKVLGYNLMQAMRPAVEEINNCSSLPGVLLGYEMDV CYLSNNIHPGLYPLAQ 120
Qy	121 DDDLLPILKDYSQYMPHVVAVIGPDNSEAITVSNILSHFLIPQITYSAISDKLRDKRHP 180
Db	121 DDDLLPILKDYSQYMPHVVAVIGPDNSEAITVSNILSHFLIPQITYSAISDKLRDKRHP 180
Qy	181 PSMLRTVPSATHHIEAMVQLMVHFQWNWIVVLVSDDDYGRENSHLLSQRLLTTS DICIAF 240
Db	181 PSMLRTVPSATHHIEAMVQLMVHFQWNWIVVLVSDDDYGRENSHLLSQRLLTTS DICIAF 240
Qy	241 QEVLPipeSSQVMRSBEEQRQLDNILDKLRRTSARVVVVFSPELSLYSFFHEVLRWNPTGP 300
Db	241 QEVLPipeSSQVMRSBEEQRQLDNILDKLRRTSARVVVVFSPELSLYSFFHEVLRWNPTGP 300
Qy	301 VWIASESWAIDPVHLNLTELRTGTPLGVTIQRVSIPGFSQPRVRRDKPGYPVPNTTNLR 360
Db	301 VWIASESWAIDPVHLNLTELRTGTPLGVTIQRVSIPGFSQPRVRRDKPGYPVPNTTNLR 360
Qy	361 TTQNQDCDACLNNTKSPNNILILSGERVVSVYSAVYAVAHRLGCNRVRCTKQKVY 420
Db	361 TTQNQDCDACLNNTKSPNNILILSGERVVSVYSAVYAVAHRLGCNRVRCTKQKVY 420
Qy	421 PWQLLREIWHVNPTLLGNRLPPDQGDMPMLLDIIQWQWDLSQNPQSIASYSPTSKRLT 480
Db	421 PWQLLREIWHVNPTLLGNRLPPDQGDMPMLLDIIQWQWDLSQNPQSIASYSPTSKRLT 480
Qy	481 YINNVSYTPNNTVPVSMCSKSCQPGQMKKSVGLHPCCPECLDCMPGTYLNRSADEPNCL 540
Db	481 YINNVSYTPNNTVPVSMCSKSCQPGQMKKSVGLHPCCPECLDCMPGTYLNRSADEPNCL 540
Qy	541 SCPGSMWSYKNDITCPQRRPTPLEHEVPTIVVAILAALGFPSTLAILPIFWRHPQTPMV 600

Db 541 SCPGSMWSYKNDITCPQRRPTFLEWHBVPТИVAILAALGPFSTLAILPIFWRHPQTPMV 600
Qy 601 RSAGGPMCPMLVPLLALPGMVPVYVGPTVPSCPCRQAPPTVCPSCICLSCITVRSPQIV 660
Db 601 RSAGGPMCPMLVPLLALPGMVPVYVGPTVPSCPCRQAPPTVCPSCICLSCITVRSPQIV 660
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Db 661 CVPKMARRLPSAYSFWMRYHGPYVVAPIATAIKVALVGNMLATTINPIGRTDPDDPNIM 720
Qy 721 ILSCHPNYRNGLLFNTSMDLLSVLGFSFAYMGKELPTNYNEAKFITLSMTPSFTSSISL 780
Db 721 ILSCHPNYRNGLLFNTSMDLLSVLGFSFAYMGKELPTNYNEAKFITLSMTPSFTSSISL 780
Qy 781 CTFMSVHDGVLVТИMDLLTVLNPLAIGLGYPGPKCYMILPYPERNTSAYFNSMIQGYTM 840
Db 781 CTFMSVHDGVLVТИMDLLTVLNPLAIGLGYPGPKCYMILPYPERNTSAYFNSMIQGYTM 840
Qy 841 RKS 843
Db 841 RKS 843

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